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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/904,994	07/13/2001	Johannes Gerardus Kusters	2000.566 US	3816

7590 06/22/2005

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EXAMINER	
PORTNER, VIRGINIA ALLEN	
ART UNIT	**PAPER NUMBER**
1645	

DATE MAILED: 06/22/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/904,994	KUSTERS ET AL.	
	Examiner	Art Unit	
	Ginny Portner	1645	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on 7/13/01.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) 23-54 is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) 23-50 and 52-54 is/are rejected.

7)☐ Claim(s) 26,37-39,43-46,49 and 51-54 is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date 8/01.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: See Continuation Sheet.

5.0.2

Continuation of Attachment(s) 6). Other: sequence letter; Notice to Comply.

DETAILED ACTION

Claims 23-54 are pending.

Information Disclosure Statement

1. The information disclosure statement filed August 7, 2001 has been considered.

Sequence Requirements

2. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

Full compliance with the sequence rules is required in response to this office action. Failure to fully comply with these requirements in the time period set forth in this office action will be held non-responsive.

3. Figures 1a, 1b and 1c show sequences, which must evidence sequence identifiers in the Brief Description of the Drawings and/or the figures. If SEQ ID Nos have already been assigned to the sequences, then these identifiers should be inserted into the Brief Description of the Drawings to place the instant Application in compliance with the sequence rules.

4. The time period set for this requirement is the time period set for this letter.

Claim Rejections - 35 USC § 101

5. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

6. Claim 30 is not an isolated and purified DNA fragment and therefore reads on a product of nature; Claim 33 depends from claim 30 and reads on a naturally occurring H. felis host cell that would comprise the DNA of claim 30; the claimed inventions of claims 30 and 33 are directed to non-statutory subject matter.

Claim Objections

7. Claim 26 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. Claim 26 is directed to the nucleic acid molecule of claim 23, which encodes one or both the urease X and urease Y subunit polypeptides, but is not required to

be of any specific coding sequence, thus broadening the scope of claim 23, which requires the claimed nucleic acid to refer to SEQ ID NO 1.

8. Claims 37-39 are objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. Claims 37-39 directly or indirectly depend from claim 34 and recite the phrase "or an immunogenic fragment of said polypeptide which induces an immune response against ureaseXY'" thus defining a polypeptide of any size that will induce an immune response, which could be as small as 10 amino acids, and therefore broadens the scope of claim 34 which requires the polypeptide to be at least 40 amino acids in length.

9. Claims 43-45 are objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. Claims 43-45 directly or indirectly depend from claim 40 and recite the phrase "or an immunogenic fragment of said polypeptide which induces an immune response against ureaseXY'" thus defining a polypeptide of any size that will induce an immune response, which could be as small as 10 amino acids, and therefore broadens the scope of claim 40 which requires the polypeptide to be at least 40 amino acids in length.

10. Claim 46 is objected to because of the following informalities: Claim 46 has been amended to depend from Claim 23, 30,31, 32, 33 or 34 or 40. The claim recites one too many "or" terms and appears to depend from more than one claim simultaneously. Appropriate correction is required.

11. Claim 49 is objected to because of the following informalities: Claim 49 recites a Markush group but in improper Markush group format. A Markush group is introduced by the phrase "selected from the group consisting of" followed by species in the format of A, B, C and D. Claim 49 recites the species in the following format A, B, C and D, E, F, G, H, I, J, K and L; this format does not set forth a proper Markush group. Appropriate correction is required.

12. Claim 51 is objected to under 37 CFR 1.75(c) as being in improper form because a multiple dependent claim should depend from other claims in the alternative and not two claims simultaneously. See MPEP § 608.01(n). Accordingly, the claim[redacted] 51 will not been further

treated on the merits. Claim 51 depends from both claims 46 and 34 ; and claim 46 and 40 simultaneously.

13. Claims 52-54 are objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form.

a. Claims 52, and 53 depend from a prior claim but do not further limit the composition from which they depend. A recited intended use does not modify a composition claim. While the specification can be used to provide definitive support, the claims are not read in a vacuum. Rather, the claim must be definite and complete in and of itself. Limitations from the specification will not be read into the claims. The claims as they stand are incomplete and fail to provide adequate structural properties to allow for one to identify what is being claimed.

b. Claim 52 recites the phrase "or a fragment thereof", which broadens the scope of claim 23 from which it depends, as the claimed nucleic acid is no longer required to be "at least 40 nucleotides" , nor is it required to encode an immunogenic fragment of the Helicobacter felis polypeptides.

c. Claims 53 recites the phrase "or a fragment thereof", which broadens the scope of claims 34 or 40 from which it depends, as the claimed polypeptide is no longer required to be "at least 40 amino acids" , nor is it required to encode an immunogenic fragment of the Helicobacter felis polypeptides.

Claim Rejections - 35 USC § 112

14. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

15. Claims 46-49 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in

the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

16. Claims 46 (depends from claims 23, 30 or 31) and 47-49 and is directed to a vaccine which comprises fragments of nucleic acid that are 40 nucleotides in length, as well as homologous nucleic acid sequences of the recited SEQ ID Nos and may be any size larger than 40 nucleotides in length, but is not required to encode any specific sequence, as long as the polypeptide is immunogenic, but need not be associated with bacterial virulence.

17. Applicant's specification fails to provide guidance to the skilled artisan on the parameters for gene delivery for the breadth of the claimed invention. Numerous factors complicate the gene therapy art which have not been shown to be overcome by routine experimentation. These include, the fate of the DNA vector itself (volume of distribution, rate of clearance into the tissues, etc.), the *in vivo* consequences of altered gene expression and protein function, the fraction of vector taken up by the target cell population, the trafficking of the genetic material within cellular organelles, the rate of degradation of the DNA, the level of mRNA produced, the stability of the mRNA produced, the amount and stability of the protein produced, and the protein's compartmentalization within the cell, or its secretory fate, once produced. These factors differ dramatically based on the vector used, the protein being produced, and the disease being treated.

Additionally, the specification does not provide any working examples which enable the claimed invention. Nor does the specification provide any guidance to the skilled artisan on how to make and use genetic constructs which would result in the desired effect. Even assuming that

an effective genetic material is constructed, it is not evident that enough cells can be transfected to provide any therapeutic benefit.

Several recent reviews indicate that efficient delivery and expression of foreign DNA has not yet been achieved by any method. Marshall (*Science*, 269:1050-1055, August, 1995) states that "there has been no unambiguous evidence that genetic treatment has produced therapeutic benefits" (page 1050, column 1) and that "difficulties in getting genes transferred efficiently to target cells- and getting them expressed- remain a nagging problem for the entire field" (page 1054, column 3). James Wilson , one skilled in the art, is quoted in the Marshall article as saying that "'[t]he actual vectors- how we're going to practice our trade- haven't been discovered yet" (page 1055, column 2). Culver et al (*TIG*, 10(5):174-178, May 1994, abstract), reviewing gene therapy for cancer, conclude that the "primary factor hampering the widespread application of gene therapy to human disease is the lack of an efficient method for delivering genes *in situ*, and developing strategies to deliver genes to a sufficient number of tumor cells to induce complete tumor regression or restore genetic health remains a challenge" (page 178). Hodgson (*Exp. Opin. Ther. Patents*, 5(5):459-468, May, 1995, abstract) discusses the drawbacks of viral transduction and chemical transfection methods, and states that "[d]eveloping the techniques used in animal models, for therapeutic use in somatic cells, has not been straightforward" (pages 459-460). Miller et al (*FASEB J.*, 9:190-199, 1995) also review the types of vectors available for *in vivo* gene therapy, and conclude that "for the long-term success as well as the widespread applicability of human gene therapy, there will have to be advances...targeting strategies outlined in this review, which are currently only at the experimental level, will have to be translated into components of safe and highly efficient delivery systems" (page 198, column 1). Therefore,

even if the specification enabled the construction of the gene delivery vehicle comprising a cell targeting element, in the absence of particular guidance, the artisan would have been required to develop *in vivo* and *ex vivo* means of practicing the claimed methods and such development in the nascent and unpredictable gene therapy art would have been considered to have necessitated undue experimentation on the part of the practitioner.

18. Claims 46-49 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for compositions the comprise immunogenic polypeptides for induction of an immune response and immunogenic fragments of 40 amino acids in length of the claimed polypeptides, as well as vaccine compositions that comprise urease XY , does not reasonably provide enablement for vaccines that comprise any immunogenic fragments of either urease X or Y for induction of a protective immune, or homologous fragments or homologous polypeptides of any size or amino acid sequence. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

19. The specification fails to teach how to formulate and use the claimed vaccines. The term "vaccine" encompasses the ability of the specific antigen to induce protective immunity to infection or disease induction. The specification teaches that the claimed antigen is recognized by antisera containing antibodies.

The specification does not provide substantive evidence that the claimed fragment vaccines are capable of inducing protective immunity. This demonstration is required for the skilled artisan to be able to use the claimed vaccines for their intended purpose of preventing infections. Without this demonstration, the skilled artisan would not be able to reasonably

predict the outcome of the administration of the claimed vaccines, i.e. would not be able to accurately predict if protective immunity has been induced. The art recognized standard for the determination of Helicobacter pylori infection is endoscopy and evaluation of tissue samples for the presence or absence of Helicobacter (see Buck et al, 1986). Data obtained from challenge experiments must demonstrate an art recognized standard of improvement over the control in order for the composition to be considered as being useful for treatment or prevention of infection and disease. This information is essential for the skilled artisan to be able to use the claimed composition (vaccines) for their intended purpose of a *Helicobacter* vaccine. Without this demonstration, the skilled artisan would not be able to reasonably predict the outcome of the administration of the claimed vaccines, i.e. would not be able to accurately predict if protective immunity has been induced.

The prior art teaches that Helicobacter pylori vaccines are unpredictable, specifically, in the type of effect they will have on preventing or treating infection; the ability to reasonably predict the capacity of a single bacterial immunogen, to induce protective immunity is problematic. In HP WORLD-WIDE, a publication from Brocades Pharma BV Leiderdorp, The Netherlands, February 1992, data was presented stating that immunization does not appear promising. Parenteral immunization of specific pathogen free mice with *H. felis* gave no protection against gastric colonization; previous oral infection only delayed colonization (Heap,K, Australia). The article also taught that "although intra-peyers patch immunization of killed *H. pylori* in rats shows that the gut mucosa can mount a vigorous immune response, oral immunization with either live or killed bacteria induced no significant serum or salival antibody response (Dunkley, M, Australia). Blaser (HP World-WIDE) also warned that because of the

possible autoimmune component of the disease the wrong vaccine could actually make things worse."

Vaccines convey protection from infection and disease and Rappuoli et al (European Journal of Gastroenterology and Hepatology, 1993, Vol.5, (suppl. 2) pages 576-578) teach that development of a vaccine against *Helicobacter pylori* would involve four major steps:

1) identification of the factors required for virulence;

2) large-scale production and characterization of the virulence factors;

3) development of appropriate animal models to test the virulence and immunogenicity of the molecules identified; and

4) identification of the type of immunity able to prevent infection and disease.

The ability to reasonably predict the capacity of a single bacterial immunogen to induce protective immunity from in vitro antibody reactivity studies is problematic. Ellis exemplifies this problem in the recitation that "the key to the problem (of vaccine development) is the identification of the at protein component of a virus or microbial pathogen that itself can elicit the production of protective antibodies"(page 572, second full paragraph). Unfortunately, the art is replete with instances where even well characterized antigens that induce an in vitro neutralizing antibody response fail to elicit in vivo protective immunity. See Boslego et al. wherein a single gonococcal pillin protein fails to elicit protective immunity even though a high level of serum antibody response is induced (page 212, bottom of column 2). Accordingly, the art indicates that it would require undue experimentation to formulate and use a successful vaccine without the prior demonstration of vaccine efficacy.

Further, the specification fails to provide an adequate written description of polypeptides that share a homology with any sequence of 40 amino acids or homologous polypeptide or any fragment that will serve as a vaccine immunogen against Helicobacter felis infection. The skilled artisan would be required to de novo locate, identify and characterize the claimed other proteins. This would require undue experimentation given the fact that the specification is completely lacking in teachings as to homologous polypeptides that are immunogenic but must also be protective with the claimed characteristics.

20. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

21. Regarding claim 23 and claims 24-33 which depend therefore and recite the phrase "such as" renders the claims indefinite because it is unclear whether the limitations following the phrase are part of the claimed invention. See MPEP § 2173.05(d). Additionally, claim 26 is rejected under 35 USC 112, second paragraph for not providing antecedent basis for the recited terms urease X and urease Y. Claim 26 depends from claim 23 which recites the phrase "two subunit polypeptides"; the terms urease X and urease Y do not evidence antecedent basis in the phrase "two subunit polypeptides".

22. Claims 34 and 35-39 which depend therefrom are rejected under 35 USC 112, second paragraph as they recite the limitation "ureaseXY" in reference to the term "urease X". There is insufficient antecedent basis for this limitation "ureaseXY" in the claim. An immunogen obtained from urease X is not required to be the same immunogen obtained from urease Y, The polypeptides of the urease X subunit are not required to induce an immune response to the urease Y subunit based upon the claim limitations recited in claim 34 and claims 35-39, therefore the claimed urease X fragment would not induce an immune response to urease Y of the recited ureaseXY polypeptide of the claims. The term immunogenic fragment of urease X does not

provide antecedent basis for an immune response to ureaseXY; "ureaseXY" therefore lacks antecedent basis in the term urease X.

23. Claims 40 and 41-45 which depend therefrom recite the limitation "ureaseXY" in reference to the term "urease Y"; there is insufficient antecedent basis for this limitation "ureaseXY" in the claim. An immunogen obtained from urease Y is not required to induce an immune response to urease X. The polypeptides in claim 40 and claims 41-45, therefore would not induce an immune response to urease X of the recited ureaseXY polypeptide recited in the claims based upon a urease Y polypeptide fragment. The term immunogenic fragment of urease Y does not provide antecedent basis for an immune response to ureaseXY; "ureaseXY" therefore lacks antecedent basis in the term urease Y.

24. Claims 23-50 and 52-54 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. All of the claims recite the term "homologous" or homology", but what this structurally means is unclear. Upon consideration of the definitions provided for this term in the instant Specification, the examiner found (paragraph [0076]) it to teach "One of the many algorithms suitable for the determination of the level of nucleic acid homology" is suggested for determining the scope of what is now claimed. In light of the definition which is "one of many", and does not provide a definite definition, but any algorithm may be used, all of the claims are indefinite as what the term homology or homologous means. Additionally, Roger Lewin and Reeck, GR et al are being cited with respect to the lack of clarity in the art with respect to what "homology" or "homologous" mean at the structural level. The term homology or homologous is understood to refer to an evolutionary relationship that does not define any specific structural correspondence between molecules. The meets and bounds of what is now claimed are unclear.

Claim Rejections - 35 USC § 102

25. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

((b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

26. Claims 23-50 and 52-54 are rejected under 35 U.S.C. 102(b) as being anticipated by Labigne et al (US Patent 5,843,460)

(**Instant claims 23-30, 46-48, and 52**) Labigne et al disclose the instantly claimed invention directed to an isolated nucleic acid of Helicobacter felis urease that encodes at least an immunogenic fragment of one of the subunits, wherein the immunogenic fragment is encoded by 40 nucleotides in length (see SEQ ID No 19, which is a nucleic acid sequence of 2619 nucleotides which shares 100% sequence identity with nucleic acids 1134-1160 of SEQ ID NO 1, as well as encodes functional homolog of the instantly claimed Helicobacter felis urease, as the Helicobacter felis urease of Labigne et al shares 85% sequence identity with SEQ ID NO 3, a subunit of the instantly claimed isolated nucleic acid. The nucleic acid of Labigne et al may be DNA (see col. 29, line 9) or RNA (see col. 12, line 54) and may further comprise adjuvants, and an additional antigen (see col. 9, lines 9-14; col. 13, lines 38-59). The DNA molecules are disclosed to function as detection reagents formulated into to kits for invitro detection of Helicobacter infection (see col. 13, lines 1-16).

While Labigne et al does not refer to the Helicobacter felis urease which comprises two subunits, as urease subunit X and Y, the disclosed Helicobacter felis urease subunits of Labigne et al anticipate the instantly claimed invention directed to Helicobacter felis urease homologs that share a nucleic acid sequence with at least 85, 90, 94 or 97 % sequence homology with SEQ ID NO 1.

(**Instant claims 31-33, 46-48**) Labigne et al disclose a recombinant DNA molecule comprising a nucleotodies sequence according to claim 23 under the control of a functionally linked promoter (see col. 13, lines 30-37). The recombinant DNA is incorporated into a live recombinant carrier, which includes viruses, baculovirus, vaccinia viruses, and transformation vectors (see col. 13, lines 44-45). Among the host cells that are transformed with the nucleic acid molecule of claim 23, the DNA fragment of claim 30, the recombinant DNA of claim 31 or the live recombinant carrier of claim 32, include E.coli, Shigellae, Salmonella, Mycobacterium tuberculosis, and eukaryotic host cells (see col. 13, lines 38-51).

(**Instant claims 34-39, 53**) Labigne et al discloses the instantly claimed Helicobacter felis polypeptide (see Labigne et al, col. 7, lines 15-32) that comprises an immunogenic fragment of SEQ ID NO 2, wherein the polypeptide is immunogenic and would induce an immune response against ureaseXY, wherein the polypeptide of SEQ ID NO 23 of Labigne et al shares 100% identity over a fragment (Labigne col. 7, lines 29-32) of SEQ ID NO 2 "KTVAQLMEE" AND "TFPDGTKL", and shares 56 identical amino acids with SEQ ID NO 2.

(**Instant claims 40-45, 53**) Labigne et al also disclose an isolated polypeptide that comprises an immunogenic fragment, wherein the polypeptide is at least 50 amino acids in length and shares at least 97% sequence homology with an amino acid sequence of SEQ ID NO 3 (see sequence alignment with extensive regions that share 100% identity with SEQ ID NO 3).). The polypeptides/proteins are disclosed for a diagnostic test for detection of Helicobacter felis infection (see col. 12, lines 2-5 "in-vitro detection" of antibodies in a sample).

(**Instant claims 46-49**) Compositions that comprise a pharmaceutically acceptable carrier (see col. 9, lines 15-22; col. 13, lines 52-59) together with a nucleic acid, or immunogenic

Helicobacter felis urease homolog, carrier or host cell (see col. 13, lines 30-59) together with an additional antigen HspA or HspB, or homolog thereof (see Labigne et al, col. 31, lines 25-50 and col. 8, lines 33-38, especially col. 31, lines 31-32) "Chlamydia" are disclosed.

Instant claim 50, 54: Compositions of anti-Helicobacter felis urease antibodies are disclosed (cross reactive, see col 9, lines 6-14) for providing passive immunity, and therefore function as vaccine compositions comprising antibodies (see Labigne et al, col. 9, lines 27-30; see col. 10, lines 62-67, col. 11, lines 1-67 and col. 12, lines 1-5). The antibodies are disclosed for a detection of Helicobacter felis urease polypeptides in a sample (see col. 10, lines 64-67 col. 11, lines 1-19 and 20-30). Labigne et al anticipates the instantly claimed invention.

Conclusion

27. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.
28. USPat.5985631, SEQ ID NO 1 discloses a homologous polypeptide fragment.
29. USPat.6039959, SEQ ID NO 2 discloses a homologous polypeptide fragment.
30. JP09087297, sequence accession number AAW16889 is cited to show a homologous polypeptide fragment with 94% identity.
31. Swiss-Prot Accession number P50043 is cited to show a polypeptide fragment homolog of the instantly claimed urease subunit from Mycobacterium tuberculosis.
32. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ginny Portner whose telephone number is (571) 272-0862. The examiner can normally be reached on M-F, alternate Fridays off.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith can be reached on (571) 272-0864.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Vgp June 9, 2005

L. F. Smith
LYNETTE R. F. SMITH
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Notice to Comply	Application No.	Applicant(s)	
	Examiner Portner	Art Unit 1645	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set in the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: Additional Sequences have been found; find narrative in attached document. Additional Sequences found in Figure 1,

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", **as well as an amendment specifically directing its entry into the application.**

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-2510
For CRF Submission Help, call (571) 272-2501/2583.
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Needs SEQIDNos

Legend to the figures

Figure 1a: Comparison of the nucleic acid sequence encoding UreX and Y, including a short non-coding region bridging the two coding sequences, from *Helicobacter felis* species CS1, Kukka, Ds4, 2301 and 390 with the nucleic acid sequence encoding UreA and B, including a short non-coding region bridging the two coding sequences, from *Helicobacter felis*, *pylori* and *heilmannii*

Figure 1b: Comparison of the amino acid sequence of UreX from *Helicobacter felis* species CS1, Kukka, Ds4, 2301 and 390 with the amino acid sequence encoding UreA from *Helicobacter felis*, *pylori* and *heilmannii*

Figure 1c: Comparison of the amino acid sequence of UreY from *Helicobacter felis* species CS1, Kukka, Ds4, 2301 and 390 with the amino acid sequence encoding UreB from *Helicobacter felis*, *pylori* and *heilmannii*

Figure 2: Polyacrylamide gel of the expression products UreX and UreY

Lane 7 : Biorad broad range marker
Lane 8 : Complete cell culture before induction (small scale culture)
Lane 9 : Complete cell culture after induction (small scale culture)
Lane 10 : Complete cell culture after induction (large scale culture)
Lane 11 : Supernatant after induction (large scale culture).
Lane 12 : Biorad pre-stained marker

[0076] The DNA can most easily be isolated from the micro-organisms present in swabs of the upper digestive tract or in the saliva of the animal to be tested. Specific primers can easily be selected from the many regions of the ureX and ureY coding sequences and the non-coding intergenic sequence that differ in sequence from the comparable regions in the ureAB coding sequences. One of the many algorithms suitable for the determination of the level of nucleic acid homology and for comparison of nucleotide sequences in general is known as "Clustal W". It has been described by Thompson et al., in Nucleic Acid Research 22: 4673-4680 (1994). The program can be found at several sites on Internet. An more recent alternative for this program is e.g. Align Plus for Windows, available from Scientific and Educational Software, P.O.Box 72045 Durham, N.C. 27722-2045, USA.

112 2nd PG Pub

Homology definition

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 15, 2005, 20:34:30 ; Search time 21.461 Seconds
(without alignments)
1975.712 Million cell updates/sec

Title: US-09-904-994B-3
Perfect score: 2999
Sequence: 1 MKMKKQEYVNTYGPTKGDKV.....KLCTSKPTSQVPLAQRYTFF 568

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 324380

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	67.5	2.3	95	4	US-09-513-999C-7491	Sequence 7491, Ap
4	66.5	2.2	89	4	US-09-107-532A-3751	Sequence 3751, Ap
5	66	2.2	96	4	US-09-270-767-36576	Sequence 36576, A
6	66	2.2	96	4	US-09-270-767-51793	Sequence 51793, A
7	65	2.2	75	4	US-09-107-532A-5840	Sequence 5840, Ap
8	64	2.1	15	3	US-09-091-001-2	Sequence 2, Appli
9	62	2.1	95	2	US-08-461-990B-26	Sequence 26, Appl
10	61.5	2.1	100	4	US-09-540-236-3479	Sequence 3479, Ap
11	60.5	2.0	79	4	US-09-198-452A-1198	Sequence 1198, Ap
12	60	2.0	82	2	US-08-773-251-22	Sequence 22, Appl
13	60	2.0	100	4	US-09-107-532A-6976	Sequence 6976, Ap
14	59.5	2.0	81	2	US-08-470-670A-10	Sequence 10, Appl
15	59.5	2.0	81	3	US-08-461-511A-10	Sequence 10, Appl
16	59.5	2.0	97	4	US-09-270-767-59857	Sequence 59857, A
17	58	1.9	52	3	US-09-187-789-46	Sequence 46, Appl
18	58	1.9	52	4	US-09-139-600-41	Sequence 41, Appl
19	58	1.9	52	4	US-09-989-903-46	Sequence 46, Appl
20	58	1.9	100	4	US-09-513-999C-6734	Sequence 6734, Ap
21	57.5	1.9	73	3	US-09-134-001C-4818	Sequence 4818, Ap
22	57	1.9	81	4	US-09-270-767-38950	Sequence 38950, A
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25	56.5	1.9	87	4	US-09-513-999C-5522	Sequence 5522, Ap
26	56.5	1.9	91	4	US-09-902-540-13686	Sequence 13686, A
27	56	1.9	60	4	US-09-107-532A-7132	Sequence 7132, Ap
28	56	1.9	69	4	US-09-270-767-40017	Sequence 40017, A
29	56	1.9	69	4	US-09-270-767-55233	Sequence 55233, A
30	56	1.9	92	2	US-09-051-589-1	Sequence 1, Appli
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32	55.5	1.9	67	4	US-09-107-532A-4027	Sequence 4027, Ap
33	55	1.8	70	3	US-09-367-953B-63	Sequence 63, Appl
34	55	1.8	79	2	US-08-997-080-87	Sequence 87, Appl
35	55	1.8	79	2	US-08-997-362-87	Sequence 87, Appl
36	55	1.8	79	3	US-08-873-970-87	Sequence 87, Appl
37	55	1.8	79	3	US-09-095-855-87	Sequence 87, Appl
38	55	1.8	79	3	US-09-324-542-87	Sequence 87, Appl
39	55	1.8	79	4	US-09-205-426-87	Sequence 87, Appl
40	55	1.8	93	4	US-09-615-192A-345	Sequence 345, App
41	54.5	1.8	60	4	US-09-732-210-809	Sequence 809, App
42	54.5	1.8	82	4	US-09-543-681A-5615	Sequence 5615, Ap
43	54.5	1.8	96	1	US-08-015-986A-7	Sequence 7, Appli
44	54.5	1.8	96	2	US-08-446-363-7	Sequence 7, Appli
45	54.5	1.8	96	4	US-09-248-796A-20403	Sequence 20403, A

ALIGNMENTS

RESULT 1
US-08-928-081-1
; Sequence 1, Application US/08928081
; Patent No. 5985631
; GENERAL INFORMATION:
; APPLICANT: Soman, Gopalan
; APPLICANT: Thomas, Jr., William D.
; APPLICANT: Monath, Thomas P.
; TITLE OF INVENTION: Stabilization of
; TITLE OF INVENTION: Helicobacter Urease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,081
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06132/023001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-928-081-1

Query Match 2.6%; Score 77; DB 2; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.6;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 211 EAGAIGFKLHEDWGT 225
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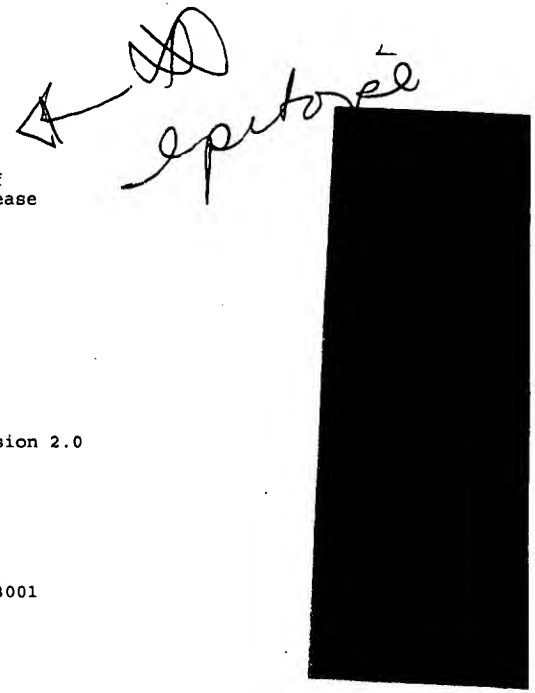

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Db          1 KLTSREMEKLMIVVAADLARRRKERGLKLNYPEAVAMITYEVLEGARDG-KTVAQLMQYG 59

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RESULT 4
US-08-467-822-23
; Sequence 23, Application US/08467822
; Patent No. 5843460
;  GENERAL INFORMATION:
;    APPLICANT:  Labigne, Agnes
;    APPLICANT:  Sauerbaum, Sebastien
;    APPLICANT:  Ferrero, Richard L.
;    APPLICANT:  Thiberge, Jean-Michel
;    TITLE OF INVENTION:  IMMUNOGENIC COMPOSITIONS AGAINST
;    TITLE OF INVENTION:  HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
;    TITLE OF INVENTION:  COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
;    TITLE OF INVENTION:  POLYPEPTIDES
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,822
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/447,177
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/432,697
;      FILING DATE:  02-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  03495.0137-02000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  100 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-467-822-23

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Db          1 MELTPREKDKLLLFTAGLVAERRLAKGLKLNYPERVALISCAIMEGAREG-KTVAQLMSE 59

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RESULT 5
US-08-432-697-23
; Sequence 23, Application US/08432697
; Patent No. 6248330
;  GENERAL INFORMATION:
;    APPLICANT:  Labigne, Agnes
;    APPLICANT:  Sauerbaum, Sebastien
;    APPLICANT:  Ferrero, Richard L.
;    APPLICANT:  Thiberge, Jean-Michel
;    TITLE OF INVENTION:  IMMUNOGENIC COMPOSITIONS AGAINST
;    TITLE OF INVENTION:  HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
;    TITLE OF INVENTION:  COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
;    TITLE OF INVENTION:  POLYPEPTIDES
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/432,697
;      FILING DATE:  02-MAY-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  03495.0137-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  100 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-432-697-23

  Query Match             22.1%;  Score 261.5;  DB 3;  Length 100;
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  Matches   56;  Conservative   17;  Mismatches   26;  Indels    1;  Gaps    1;

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RESULT 6
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; Sequence 23, Application US/08466248
; Patent No. 6258359
;  GENERAL INFORMATION:
;    APPLICANT:  Labigne, Agnes
;    APPLICANT:  Sauerbaum, Sebastien
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DB:                    4              Gaps:          0

US-09-904-994B-3 (1-568) x US-09-431-705-1 (1-4824)

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RESULT 4
US-09-431-705-19
; Sequence 19, Application US/09431705
; Patent No. 6585975
; GENERAL INFORMATION:
;  APPLICANT:  Kleanthous, Harold
;  APPLICANT:  Londono-Arcila, Patricia
;  APPLICANT:  Freeman, Donna
;  TITLE OF INVENTION:  Use of salmonella vectors for
;  TITLE OF INVENTION:  vaccination against helicobacter infection
;  FILE REFERENCE:  06132/060001
;  CURRENT APPLICATION NUMBER: US/09/431,705
;  CURRENT FILING DATE:  1999-11-01
;  NUMBER OF SEQ ID NOS:  52
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 4824
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: includes sequences from Helicobacter pylori,
;   OTHER INFORMATION: Salmonella typhimurium, and Escherichia coli
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;   LOCATION: (3893)...(3934)
;   NAME/KEY: CDS
;   LOCATION: (3938)...(4027)
;   NAME/KEY: CDS
;   LOCATION: (4031)...(4285)
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;   LOCATION: (4289)...(4300)
;   NAME/KEY: CDS
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;   NAME/KEY: CDS
;   LOCATION: (4673)...(4711)
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;   LOCATION: (4784)...(4824)
US-09-431-705-19

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US-09-904-994B-3 (1-568) x US-09-431-705-19 (1-4824)

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RESULT 5
US-08-467-822-19
; Sequence 19, Application US/08467822
; Patent No. 5843460
;  GENERAL INFORMATION:
;    APPLICANT:  Labigne, Agnes
;    APPLICANT:  Sauerbaum, Sebastien
;    APPLICANT:  Ferrero, Richard L.
;    APPLICANT:  Thiberge, Jean-Michel
;    TITLE OF INVENTION:  IMMUNOGENIC COMPOSITIONS AGAINST
;    TITLE OF INVENTION:  HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
;    TITLE OF INVENTION:  COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
;    TITLE OF INVENTION:  POLYPEPTIDES
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,822
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/447,177
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/432,697
;      FILING DATE:  02-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  03495.0137-02000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2619 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  31..36
;      OTHER INFORMATION:  /standard_name= "Shine-Dalgarno
;      OTHER INFORMATION:  sequence."
;    FEATURE:
;      NAME/KEY:  misc_feature
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;      OTHER INFORMATION:  sequence."
US-08-467-822-19

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Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            3.17%          Indels:        0
DB:                     2              Gaps:          0

US-09-904-994B-3 (1-568) x US-08-467-822-19 (1-2619)

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Qy        222 AspTrpGlyThrThrProSerAlaIleAspHisCysLeuSerValAlaAspGluTyrAsp 241

Db       1472 GACTGGGGCACCACTCCTTCTGCAATCAATCATGCGTTAGATGTTGCGGACAAATACGAT 1531

Qy        242 ValGlnValCysIleHisThrAspThrValAsnGluAlaGlyTyrValAspAspThrLeu 261

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Qy        262 AsnAlaMetAsnGlyArgAlaIleHisAlaTyrHisIleGluGlyAlaGlyGlyGlyHis 281

Db       1592 GCTGCTATTGCTGGACGCACTATGCACACTTTCCACACTGAAGGCGCTGGCGGCGGACAC 1651

Qy        282 SerProAspValIleThrMetAlaGlyGluLeuAsnIleLeuProSerSerThrThrPro 301

Db       1652 GCTCCTGATATTATTAAAGTAGCCGGTGAACACAACATTCTTCCCGCTTCCACTAACCCC 1711

Qy        302 ThrIleProTyrThrIleAsnThrValAlaGluHisLeuAspMetLeuMetThrCysHis 321

Db       1712 ACCATCCCTTTCACCGTGAATACAGAAGCAGAGCACATGGACATGCTTATGGTGTGCCAC 1771

Qy        322 HisLeuAspLysArgIleArgGluAspLeuGlnPheSerGlnSerArgIleArgProGly 341

Db       1772 CACTTGGATAAAAGCATTAAAGAAGATGTTCAGTTCGCTGATTCAAGGATCCGCCCTCAA 1831

Qy        342 SerIleAlaAlaGluAspValLeuHisAspMetGlyValIleAlaMetThrSerSerAsp 361

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Qy        382 AsnLysLysGluPheGlyLysLeuProGluAspGlyLysAspAsnAspAsnPheArgIle 401

Db       1952 AACAAGAAAGAATTTGGCCGCTTGAAAGAAGAAAAAGGCGATAACGACAACTTCAGGATC 2011

Qy        402 LysArgTyrIleSerLysTyrThrIleAsnProAlaLeuThrHisGlyValSerGluTyr 421

Db       2012 AAACGCTACTTGTCTAAATACACCATTAACCCAGCGATCGCTCATGGGATTAGCGAGTAT 2071

Qy        422 IleGlySerValGluGluGlyLysIleAlaAspLeuValValTrpAsnProAlaPhePhe 441

Db       2072 GTAGGTTCAGTAGAAGTGGGCAAAGTGGCTGACTTGGTATTGTGGAGTCCAGCATTCTTT 2131

Qy        442 GlyValLysProLysIleValIleLysGlyGlyMetValValPheSerGluMetGlyAsp 461

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Db       2192 GCGAACGCTTCTATCCCTACCCCACAACCGGTTTATTACAGAGAAATGTTCGCTCATCAT 2251

Qy        482 GlyLysAlaLysPheAspThrSerIleThrPheValSerLysValAlaTyrGluAsnGly 501

Db       2252 GGTAAAGCTAAATACGATGCAAACATCACTTTTGTGTCTCAAGCGGCTTATGACAAAGGC 2311

Qy        502 ValLysGluLysLeuGlyLeuGluArgGlnValLeuProValLysAsnCysArgAsnIle 521

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Qy        562 AlaGlnArgTyrThrPhePhe 568

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RESULT 5
US-08-467-822-19
; Sequence 19, Application US/08467822
; Patent No. 5843460
; GENERAL INFORMATION:
; APPLICANT: Labigne, Agnes
; APPLICANT: Sauerbaum, Sebastien
; APPLICANT: Ferrero, Richard L.
; APPLICANT: Thiberge, Jean-Michel
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
; TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,822
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,177
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,697
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0137-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2619 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..36
; OTHER INFORMATION: /standard_name= "Shine-Dalgarno
; OTHER INFORMATION: sequence."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 756..759
; OTHER INFORMATION: /standard_name= "Shine-Dalgarno
; OTHER INFORMATION: sequence."
US-08-467-822-19

Alignment Scores:
Pred. No.: 5.14e-241 Length: 2619
Matches: 411
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Percent Similarity: 85.01% Conservative: 71
Best Local Similarity: 72.49% Mismatches: 85
Query Match: 74.82% Indels: 0
DB: 2 Gaps: 0

US-09-904-994B-3 (1-568) x US-08-467-822-19 (1-2619)

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Qy          2 LysMetLysLysGlnGluTyrValAsnThrTyrGlyProThrLysGlyAspLysValArg 21
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Db        772 AAGATTTCACGAAAAGAATATGTTTCTATGTATGGTCCCACTACCGGGGATCGTGTTAGA 831

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              ||||||||||||||||||      ||||||||||||||   ||||||||||||||||||
Db        832 CTCGGCGACACTGATTTGATCTTAGAAGTGGAGCATGATTGCACCACTTATGGTGAAGAG 891

Qy         42 LeuLysPheGlyAlaGlyLysThrIleArgGluGlyMetGlyGlnSerAsnSerProAsp 61
              :::|||||||||   ||||||||||||||::::||||||   |||:::||||||||||
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Db        952 TCTTATGAATTAGATTTGGTGCTCACTAACGCCCTCATTGTGGACTATACGGGCATTTAC 1011

Qy         82 LysAlaAspIleGlyIleLysAsnGlyLysIleHisGlyIleGlyLysAlaGlyAsnLys 101
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Db       1012 AAAGCCGACATTGGGATTAAAGACGGCAAGATTGCAGGCATTGGCAAGGCAGGCAATAAG 1071

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              ||||||||||||||||||      ::::::   ||||||      ||||||||||||||||
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Db       1252 CCTGCGGATGGCACGAATGCGACCACCATCACTCCCGGACGCGCTAATCTAAAAAGTATG 1311

Qy        182 LeuArgAlaAlaGluGluTyrSerMetAsnValGlyPheLeuGlyLysGlyAsnSerSer 201
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Db       1312 TTGCGTGCAGCCGAAGAATACGCCATGAATCTAGGCTTTTTGGCTAAGGGGAATGTGTCT 1371

Qy        202 SerLysLysGlnLeuValGluGlnValGluAlaGlyAlaIleGlyPheLysLeuHisGlu 221
                 :::      |||   :::|||:::||||||||||||||||||||:::||||||
Db       1372 TACGAACCCTCTTTACGCGATCAGATTGAAGCAGGGGCGATTGGTTTTAAAATCCACGAA 1431

Qy        222 AspTrpGlyThrThrProSerAlaIleAspHisCysLeuSerValAlaAspGluTyrAsp 241
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Db       1432 GACTGGGGAAGCACACCTGCAGCTATTCACCACTGCCTCAATGTCGCCGATGAATACGAT 1491

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Db       1492 GTGCAAGTGGCTATCCACACCGATACCCTTAACGAGGCGGGCTGTGTAGAAGACACCCTA 1551

Qy        262 AsnAlaMetAsnGlyArgAlaIleHisAlaTyrHisIleGluGlyAlaGlyGlyGlyHis 281
                 |||:::   ||||||   ||||||   :::|||   ||||||||||||||||||||||
Db       1552 GAGGCGATTGCCGGGCGCACCATCCATACCTTCCACACTGAAGGGGCTGGGGGTGGACAC 1611

Qy        282 SerProAspValIleThrMetAlaGlyGluLeuAsnIleLeuProSerSerThrThrPro 301
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Db       1612 GCTCCAGATGTTATCAAAATGGCAGGGGAATTTAACATTCTACCCGCCTCTACTAACCCG 1671

Qy        302 ThrIleProTyrThrIleAsnThrValAlaGluHisLeuAspMetLeuMetThrCysHis 321
              ||||||||||:|||   ||||||   |||||||||:::||||||||||||   ||||||
Db       1672 ACCATTCCTTTCACCAAAAACACTGAAGCCGAGCACATGGACATGTTAATGGTGTGCCAC 1731

Qy        322 HisLeuAspLysArgIleArgGluAspLeuGlnPheSerGlnSerArgIleArgProGly 341
              ||||||||||||   |||:::||||||:::||||||:::   ||||||||||||||||
Db       1732 CACTTGGATAAAAGTATCAAGGAAGATGTGCAGTTTGCCGATTCGAGGATTCGCCCCCAA 1791

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Qy        362 SerGlnAlaMetGlyArgAlaGlyGluValIleProArgThrTrpGlnThrAlaAspLys 381
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Db       1852 TCTCAGGCTATGGGACGCGTAGGCGAGGTGATCACACGCACTTGGCAGACAGCAGACAAA 1911

Qy        382 AsnLysLysGluPheGlyLysLeuProGluAspGlyLysAspAsnAspAsnPheArgIle 401
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Db       1912 AACAAAAAAGAGTTTGGGCGCTTGAAAGAGGAAAAAGGCGATAACGACAACTTCCGCATC 1971

Qy        402 LysArgTyrIleSerLysTyrThrIleAsnProAlaLeuThrHisGlyValSerGluTyr 421
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Db       1972 AAACGCTACATCTCTAAATACACCATCAACCCCGGGATCGCGCATGGGATTTCTGACTAT 2031

Qy        422 IleGlySerValGluGluGlyLysIleAlaAspLeuValValTrpAsnProAlaPhePhe 441
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Db       2032 GTGGGCTCTGTGGAAGTGGGCAAATACGCCGACCTCGTGCTTTGGAGTCCGGCTTTCTTT 2091

Qy        442 GlyValLysProLysIleValIleLysGlyGlyMetValValPheSerGluMetGlyAsp 461
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Qy        482 GlyLysAlaLysPheAspThrSerIleThrPheValSerLysValAlaTyrGluAsnGly 501
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Db       2272 ATCAAAGAAGAACTAGGGCTAGATCGCGCGGCACCGCCAGTGAAAAACTGTCGCAATATC 2331

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RESULT 6
US-08-432-697-19
; Sequence 19, Application US/08432697
; Patent No. 6248330
; GENERAL INFORMATION:
; APPLICANT: Labigne, Agnes
; APPLICANT: Sauerbaum, Sebastien
; APPLICANT: Ferrero, Richard L.
; APPLICANT: Thiberge, Jean-Michel
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
; TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:

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ALIGNMENTS

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RESULT 1
US-08-467-822-19
; Sequence 19, Application US/08467822
; Patent No. 5843460
; GENERAL INFORMATION:
;    APPLICANT:  Labigne, Agnes
;    APPLICANT:  Sauerbaum, Sebastien
;    APPLICANT:  Ferrero, Richard L.
;    APPLICANT:  Thiberge, Jean-Michel
;    TITLE OF INVENTION:  IMMUNOGENIC COMPOSITIONS AGAINST
;    TITLE OF INVENTION:  HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
;    TITLE OF INVENTION:  COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
;    TITLE OF INVENTION:  POLYPEPTIDES
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,822
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/447,177
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/432,697
;      FILING DATE:  02-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  03495.0137-02000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2619 base pairs
;      TYPE:  nucleic acid
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;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  31..36
;       OTHER INFORMATION:  /standard_name= "Shine-Dalgarno
;       OTHER INFORMATION:  sequence."
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US-08-467-822-19

  Query Match              0.9%;  Score 27;  DB 2;  Length 2619;
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  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-08-432-697-19
; Sequence 19, Application US/08432697
; Patent No. 6248330
;  GENERAL INFORMATION:
;     APPLICANT:  Labigne, Agnes
;     APPLICANT:  Sauerbaum, Sebastien
;     APPLICANT:  Ferrero, Richard L.
;     APPLICANT:  Thiberge, Jean-Michel
;     TITLE OF INVENTION:  IMMUNOGENIC COMPOSITIONS AGAINST
;     TITLE OF INVENTION:  HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
;     TITLE OF INVENTION:  COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
;     TITLE OF INVENTION:  POLYPEPTIDES
;     NUMBER OF SEQUENCES:  44
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;       ADDRESSEE:  Dunner
;       STREET:  1300 I Street, N.W.
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20005-3315
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/432,697
;       FILING DATE:  02-MAY-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Meyers, Kenneth J.
;       REGISTRATION NUMBER:  25,146
;       REFERENCE/DOCKET NUMBER:  03495.0137-00000
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 408-4000
;       TELEFAX:  (202) 408-4400
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2619 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  31..36
;       OTHER INFORMATION:  /standard_name= "Shine-Dalgarno
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            ZIP: 02354
      COMPUTER READABLE FORM:
            MEDIUM TYPE: CD/ROM ISO9660
            COMPUTER: PC
            OPERATING SYSTEM: <Unknown>
            SOFTWARE: ASCII
      CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/107,532A
            FILING DATE: 30-Jun-1998
      PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 60/085,598
            FILING DATE: 14 May 1998
            APPLICATION NUMBER: 60/051571
            FILING DATE: July 2, 1997
      ATTORNEY/AGENT INFORMATION:
            NAME: Ariniello, Pamela Deneke
            REGISTRATION NUMBER: 40,489
            REFERENCE/DOCKET NUMBER: GTC-012
      TELECOMMUNICATION INFORMATION:
            TELEPHONE: (781)893-5007
            TELEFAX: (781)893-8777
   INFORMATION FOR SEQ ID NO: 5840:
      SEQUENCE CHARACTERISTICS:
            LENGTH: 75 amino acids
            TYPE: amino acid
            TOPOLOGY: linear
      MOLECULE TYPE: protein
      HYPOTHETICAL: YES
      ORIGINAL SOURCE:
            ORGANISM: Enterococcus faecium
      FEATURE:
            NAME/KEY:  misc_feature
            LOCATION: (B) LOCATION 1...75
      SEQUENCE DESCRIPTION: SEQ ID NO: 5840:
US-09-107-532A-5840

  Query Match              2.2%;  Score 65;  DB 4;  Length 75;
  Best Local Similarity   29.9%;  Pred. No. 1.3e+02;
  Matches   23;  Conservative   18;  Mismatches   33;  Indels    8;  Gaps    2;

Qy        483 KAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKTF 542
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Db          7 KAKEEIT---MAKVCYFTGRKIKSGNNR-----SHAMNSTKRTVKPNLQKVRVMVDGKPK 58

Qy        543 EVFVDGKLCTSKPTSQV 559
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Db         59 KVWVSTRALKSGKVERV 75
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RESULT 8
US-09-091-001-2
; Sequence 2, Application US/09091001
; Patent No. 6039959
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Treatment and Diagnosis of Infections due to
;    TITLE OF INVENTION:  Helicobacter pylori
;    NUMBER OF SEQUENCES:  13
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/091,001
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB96/02907
;      FILING DATE:
;      APPLICATION NUMBER:  GB 9524934.8
;      FILING DATE:  06-DEC-1995
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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US Pat 6039959

60

; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-091-001-2

Query Match 2.1%; Score 64; DB 3; Length 15;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy        422 IGSVEEGKIADLVVW 436
              :|||| ||:||||:|
Db          1 VGSVEVGKVADLVLW 15
```

RESULT 9
US-08-461-990B-26
; Sequence 26, Application US/08461990B
; Patent No. 5851810
; GENERAL INFORMATION:
; APPLICANT: JOHN S. BLANCHARD
; TITLE OF INVENTION: NUCLEIC ACID ENCODING RHODOCOCCUS
; TITLE OF INVENTION: PHENYLALANINE DEHYDROGENASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,990B
; FILING DATE: JUNE 5, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG J. ARNOLD
; REGISTRATION NUMBER: 34,287
; REFERENCE/DOCKET NUMBER: 96700/370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PROTEIN
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: B. STEAROTHERMOPHILUS
; INDIVIDUAL ISOLATE: ALANINE DEHYDROGENASE
US-08-461-990B-26

Query Match 2.1%; Score 62; DB 2; Length 95;
Best Local Similarity 30.6%; Pred. No. 3.7e+02;
Matches 22; Conservative 9; Mismatches 19; Indels 22; Gaps 4;

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Qy        107 VSPHMVVGVGTEAL----AGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGP 162
              |:  | | || : |     |:::: ||:                 :  |  |: ||||
Db         28 VAGRMSVQVGAQFLEKPHGGKCILL--GGV-------------PGVRRGKVTIIGGGTA- 71

Qy        163 VDGTNATTITPG 174
              ||||  |  |
Db         72 --GTNAAKIGVG 81
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